```
                    GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on:          November 24, 2003, 15:54:12 ; Search time 10684 Seconds
                                          (without alignments)
                                          11525.456 Million cell updates/sec


Title:           US-10-058-945-1
Perfect score:   3010
Sequence:        1 attgcggggcttactgcgct..........ccagaaatccctcaaggcgg 3010

Scoring table:   IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched:        2888711 seqs, 20454813386 residues

Total number of hits satisfying chosen parameters:       5777422

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :       GenEmbl:*
                 1:   gb_ba:*
                 2:   gb_htg:*
                 3:   gb_in:*
                 4:   gb_om:*
                 5:   gb_ov:*
                 6:   gb_pat:*
                 7:   gb_ph:*
                 8:   gb_pl:*
                 9:   gb_pr:*
                 10:  gb_ro:*
                 11:  gb_sts:*
                 12:  gb_sy:*
                 13:  gb_un:*
                 14:  gb_vi:*
                 15:  em_ba:*
                 16:  em_fun:*
                 17:  em_hum:*
                 18:  em_in:*
                 19:  em_mu:*
                 20:  em_om:*
                 21:  em_or:*
                 22:  em_ov:*
                 23:  em_pat:*
                 24:  em_ph:*
                 25:  em_pl:*
                 26:  em_ro:*
                 27:  em_sts:*
```

Also searched

SEQ ID NO:1 as an OLIGOMER
and using the protein, SEQ ID NO:2,
in DNA databases.
But no better art than
found here.

particularly USPAP 2002/0197605
Nakagawa et al.

```
            28:   em_un:*
        ,   29:   em_vi:*
            30:   em_htg_hum:*
            31:   em_htg_inv:*
            32:   em_htg_other:*
            33:   em_htg_mus:*
            34:   em_htg_pln:*
            35:   em_htg_rod:*
            36:   em_htg_mam:*
            37:   em_htg_vrt:*
            38:   em_sy:*
            39:   em_htgo_hum:*
            40:   em_htgo_mus:*
            41:   em_htgo_other:*
```

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

<div align="center">SUMMARIES</div>

Result No.	Score	% Query Match	Length	DB	ID	Description
1	3010	100.0	320550	1	AP005282	AP005282 Corynebac
2	3010	100.0	349980	6	AX127152	AX127152 Sequence
3	2326.6	77.3	2369	6	AX353377	AX353377 Sequence
4	2326.6	77.3	2369	6	BD106978	BD106978 L-Glutami
5	1578	52.4	1578	6	AX063735	AX063735 Sequence
6	1578	52.4	1578	6	AX469840	AX469840 Sequence
7	1546	51.4	1546	6	AX063737	AX063737 Sequence
8	1455	48.3	1455	6	AX122970	AX122970 Sequence
9	1455	48.3	1455	6	BD165087	BD165087 Novel pol
10	1405.6	46.7	2817	6	AR216136	AR216136 Sequence
11	1405.6	46.7	2817	6	AX137526	AX137526 Sequence
12	1405.6	46.7	2817	6	AX236994	AX236994 Sequence
13	1405.6	46.7	2817	6	AX322482	AX322482 Sequence
14	1405.6	46.7	2817	6	BD013817	BD013817 Novel nuc
15	1294	43.0	300330	1	AP005222	AP005222 Corynebac
16	730	24.3	1971	6	AX707003	AX707003 Sequence
17	615.4	20.4	1869	1	AF326510	AF326510 Corynebac
18	615.4	20.4	1909	6	AR216137	AR216137 Sequence
19	615.4	20.4	1909	6	AX137528	AX137528 Sequence
20	615.4	20.4	1909	6	AX236996	AX236996 Sequence
21	615.4	20.4	1909	6	AX322484	AX322484 Sequence
22	615.4	20.4	1909	6	BD013818	BD013818 Novel nuc
23	609	20.2	609	6	AX064867	AX064867 Sequence
24	609	20.2	609	6	AX469850	AX469850 Sequence
25	513	17.0	513	6	AX122971	AX122971 Sequence
26	513	17.0	513	6	BD165088	BD165088 Novel pol
27	482	16.0	1590	6	AX064869	AX064869 Sequence
28	482	16.0	1590	6	AX066975	AX066975 Sequence
29	482	16.0	1590	6	AX469852	AX469852 Sequence
30	459	15.2	1503	6	AX122968	AX122968 Sequence
31	459	15.2	1503	6	BD165085	BD165085 Novel pol
32	327	10.9	327	6	AX122969	AX122969 Sequence
33	327	10.9	327	6	BD165086	BD165086 Novel pol

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OM nucleic - nucleic search, using sw model

Run on: November 24, 2003, 14:41:25 ; Search time 750 Seconds
                                              (without alignments)
                                              10833.745 Million cell updates/sec

Title: US-10-058-945-1
Perfect score: 3010
Sequence: 1 attgcggggcttactgcgct..........ccagaaatccctcaaggcgg 3010

Scoring table: IDENTITY_NUC
                  Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   N_Geneseq_19Jun03:*
                  1:   /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1980.DAT:*
                  2:   /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1981.DAT:*
                  3:   /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1982.DAT:*
                  4:   /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1983.DAT:*
                  5:   /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1984.DAT:*
                  6:   /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1985.DAT:*
                  7:   /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1986.DAT:*
                  8:   /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1987.DAT:*
                  9:   /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1988.DAT:*
                  10: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1989.DAT:*
                  11: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1990.DAT:*
                  12: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1991.DAT:*
                  13: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1992.DAT:*
                  14: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1993.DAT:*
                  15: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1994.DAT:*
                  16: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1995.DAT:*
                  17: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1996.DAT:*
                  18: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1997.DAT:*
                  19: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1998.DAT:*
                  20: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1999.DAT:*
                  21: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2000.DAT:*
                  22: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2001A.DAT:*
                  23: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2001B.DAT:*
                  24: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2002.DAT:*
                  25: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2003.DAT:*

    Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	3010	100.0	3010	24	AAL48965	C glutamicum otsA
	2	3010	100.0	349980	22	AAH68533	C glutamicum codin
	3	2326.6	77.3	2369	24	ABK15556	DNA encoding treha
	4	1578	52.4	1578	22	AAF71761	Corynebacterium gl
	5	1578	52.4	1578	24	ABS65356	DNA encoding C. gl
	6	1546	51.4	1546	22	AAF71762	Corynebacterium gl
	7	1455	48.3	1455	22	AAH67851	C glutamicum codin
	8	1405.6	46.7	2817	22	AAF61246	C. glutamicum ATCC
	9	1405.6	46.7	2817	22	AAH49349	C. glutamicum ATCC
	10	1405.6	46.7	2817	24	ABA05864	Corynebacterium gl
	11	730	24.3	1971	25	ABZ58585	Corynebacterium gl
	12	615.4	20.4	1909	22	AAF61247	C. glutamicum ATCC
	13	615.4	20.4	1909	22	AAH49350	C. glutamicum ATCC
	14	615.4	20.4	1909	24	ABA05865	Corynebacterium gl
	15	609	20.2	609	22	AAF72327	Corynebacterium gl
	16	609	20.2	609	24	ABS65361	DNA encoding C. gl
	17	513	17.0	513	22	AAH67852	C glutamicum codin
	18	482	16.0	1590	22	AAF72328	Corynebacterium gl
	19	482	16.0	1590	22	AAF68021	Corynebacterium gl
	20	482	16.0	1590	24	ABS65362	DNA encoding C. gl
	21	459	15.2	1503	22	AAH67849	C glutamicum codin
	22	327	10.9	327	22	AAH67850	C glutamicum codin
	23	302.4	10.0	1503	22	AAH52074	Mycobacterium tube
	24	302.4	10.0	4403765	22	AAI99683	Mycobacterium tube
	25	302.4	10.0	4411529	22	AAI99682	Mycobacterium tube
	26	276	9.2	37716	23	AAS59553	Propionibacterium
	27	230	7.6	891	22	AAF72322	Corynebacterium gl
	28	230	7.6	891	24	ABS65357	DNA encoding C. gl
	29	130	4.3	768	22	AAH67853	C glutamicum codin
	30	118.4	3.9	2430	24	ABS51410	cDNA encoding larv
	31	118.4	3.9	2903	23	ABL05149	Drosophila melanog
c	32	118.4	3.9	6435	23	ABL05148	Drosophila melanog
	33	112.6	3.7	1500	21	AAZ45000	Synechocystis sp.
	34	110	3.7	534720	19	AAV30458	Rhizobium species
	35	110	3.7	536165	19	AAV30459	Rhizobium species
c	36	108.6	3.6	534720	19	AAV30458	Rhizobium species
c	37	108.6	3.6	536165	19	AAV30459	Rhizobium species
	38	104.2	3.5	303	24	ABN26396	Human ORFX polynuc
	39	98.8	3.3	1910	19	AAV02740	S. lepidophylla tr
	40	98.8	3.3	3223	19	AAV02739	S. lepidophylla tr
	41	94.8	3.1	2695	21	AAA39756	H. polymorpha TPS1
	42	94.6	3.1	1534	18	AAV00136	Trehalose-6-phosph
	43	94.6	3.1	1534	18	AAV00084	Yeast trehalose-6-
	44	94.4	3.1	831	20	AAZ10777	Trehalose-6-phosph
	45	92.8	3.1	2829	24	ABZ14682	Arabidopsis thalia

ALIGNMENTS

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OM nucleic - nucleic search, using sw model

Run on: November 24, 2003, 22:24:06 ; Search time 978 Seconds
                                              (without alignments)
                                              10067.526 Million cell updates/sec

Title: US-10-058-945-1
Perfect score: 3010
Sequence: 1 attgcggggcttactgcgct...........ccagaaatccctcaaggcgg 3010

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 2172232 seqs, 1635554964 residues

Total number of hits satisfying chosen parameters: 4344464

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Published_Applications_NA:*
                 1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
                 2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
                 3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
                 4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
                 5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
                 6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
                 7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
                 8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
                 9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
                 10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
                 11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
                 12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
                 13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
                 14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
                 15: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
                 16: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
                 17: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

      Pred. No. is the number of results predicted by chance to have a
      score greater than or equal to the score of the result being printed,
      and is derived by analysis of the total score distribution.

                              SUMMARIES
                      %
Result   Query
   No.   Score Match Length DB   ID   Description

```
    1     3010   100.0    3010   13   US-10-058-945-1           Sequence 1, Appli
    2     3010   100.0 3309400   10   US-09-738-626-1           Sequence 1, Appli
    3   2326.6    77.3    2369   10   US-09-895-382-29          Sequence 29, Appl
    4     1455    48.3    1455   10   US-09-738-626-2886        Sequence 2886, Ap
    5   1405.6    46.7    2817   10   US-09-951-536-1           Sequence 1, Appli
    6   1405.6    46.7    2817   10   US-09-963-521-1           Sequence 1, Appli
    7   1405.6    46.7    2817   10   US-09-834-721-1           Sequence 1, Appli
    8   1405.6    46.7    2817   10   US-09-783-388-1           Sequence 1, Appli
    9   1405.6    46.7    2817   11   US-09-951-535-1           Sequence 1, Appli
   10      730    24.3    1971   14   US-10-212-219-1           Sequence 1, Appli
   11    615.4    20.4    1909   10   US-09-951-536-3           Sequence 3, Appli
   12    615.4    20.4    1909   10   US-09-963-521-3           Sequence 3, Appli
   13    615.4    20.4    1909   10   US-09-834-721-3           Sequence 3, Appli
   14    615.4    20.4    1909   10   US-09-783-388-3           Sequence 3, Appli
   15    615.4    20.4    1909   11   US-09-951-535-3           Sequence 3, Appli
   16      513    17.0     513   10   US-09-738-626-2887        Sequence 2887, Ap
   17      459    15.2    1503   10   US-09-738-626-2884        Sequence 2884, Ap
   18      327    10.9     327   10   US-09-738-626-2885        Sequence 2885, Ap
   19    302.4    10.0    1503   10   US-09-712-363-128         Sequence 128, App
   20      130     4.3     768   10   US-09-738-626-2888        Sequence 2888, Ap
   21      110     3.7  536165   11   US-09-939-964-1           Sequence 1, Appli
c  22    108.6     3.6  536165   11   US-09-939-964-1           Sequence 1, Appli
   23     92.8     3.1    2829   10   US-09-938-842A-2487       Sequence 2487, Ap
   24     89.4     3.0     261    9   US-09-867-550-445        Sequence 445, App
   25       82     2.7    2598   10   US-09-938-842A-1646       Sequence 1646, Ap
   26     70.2     2.3    2589   10   US-09-938-842A-1345       Sequence 1345, Ap
   27     68.4     2.3    1389   14   US-10-156-761-3920        Sequence 3920, Ap
   28     68.4     2.3 9025608   14   US-10-156-761-1           Sequence 1, Appli
   29     66.8     2.2     654   15   US-10-307-723-36          Sequence 36, Appl
   30     62.8     2.1     498   12   US-10-259-165-417         Sequence 417, App
   31     62.8     2.1     501   12   US-10-259-165-81          Sequence 81, Appl
   32     62.8     2.1    3414   12   US-10-259-165-329         Sequence 329, App
c  33     54.2     1.8     791    9   US-09-770-445-847        Sequence 847, App
   34     50.4     1.7    2621    8   US-08-779-460B-1         Sequence 1, Appli
   35     44.6     1.5    1098   14   US-10-156-761-2932        Sequence 2932, Ap
c  36     44.6     1.5 9025608   14   US-10-156-761-1           Sequence 1, Appli
   37     44.4     1.5     651   14   US-10-156-761-2671        Sequence 2671, Ap
c  38     40.8     1.4     488   11   US-09-770-961-736         Sequence 736, App
   39     40.2     1.3     256   10   US-09-878-574-9432        Sequence 9432, Ap
   40     39.8     1.3     984   14   US-10-128-714-7296        Sequence 7296, Ap
   41     39.8     1.3    1028   14   US-10-128-714-6296        Sequence 6296, Ap
   42     39.8     1.3    2882   14   US-10-128-714-296         Sequence 296, App
   43     39.8     1.3    3028   14   US-10-128-714-5296        Sequence 5296, Ap
c  44     39.4     1.3    7758   12   US-10-311-455-1076        Sequence 1076, Ap
   45     39.2     1.3    4203   10   US-09-880-107-3422        Sequence 3422, Ap
```

ALIGNMENTS

RESULT 1
US-10-058-945-1
; Sequence 1, Application US/10058945
; Publication No. US20020192674A1
; GENERAL INFORMATION:
; APPLICANT: HERMANN, Thomas
; APPLICANT: WOLF, Andreas

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OM nucleic - nucleic search, using sw model

Run on: November 24, 2003, 18:28:16 ; Search time 5588 Seconds
                                              (without alignments)
                                              13091.710 Million cell updates/sec

Title: US-10-058-945-1
Perfect score: 3010
Sequence: 1 attgcggggcttactgcgct..........ccagaaatccctcaaggcgg 3010

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   EST:*
                 1:   em_estba:*
                 2:   em_esthum:*
                 3:   em_estin:*
                 4:   em_estmu:*
                 5:   em_estov:*
                 6:   em_estpl:*
                 7:   em_estro:*
                 8:   em_htc:*
                 9:   gb_est1:*
                 10: gb_est2:*
                 11: gb_htc:*
                 12: gb_est3:*
                 13: gb_est4:*
                 14: gb_est5:*
                 15: em_estfun:*
                 16: em_estom:*
                 17: em_gss_hum:*
                 18: em_gss_inv:*
                 19: em_gss_pln:*
                 20: em_gss_vrt:*
                 21: em_gss_fun:*
                 22: em_gss_mam:*
                 23: em_gss_mus:*
                 24: em_gss_pro:*
                 25: em_gss_rod:*
                 26: em_gss_phg:*
                 27: em_gss_vrl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
	1	138.6	4.6	645	12	BM869320	BM869320 mgns004xF
c	2	122	4.1	549	28	AQ399488	AQ399488 mgxb0015E
	3	111.8	3.7	583	9	AI109201	AI109201 GH08323.5
	4	109.6	3.6	404	13	BU644825	BU644825 mgns016xP
	5	100.4	3.3	441	9	AA783493	AA783493 c5f08a1.r
c	6	98.4	3.3	1024	28	AF075787	AF075787 AF075787
	7	92.4	3.1	601	12	BI941513	BI941513 dg20h04.y
	8	91.2	3.0	436	10	BF050405	BF050405 EST435563
	9	90.2	3.0	556	12	BM869415	BM869415 mgns006xI
	10	88.2	2.9	565	12	BI941469	BI941469 dg07a02.y
	11	87.4	2.9	509	12	BM870625	BM870625 mgns011xC
	12	87.4	2.9	604	12	BM871676	BM871676 mgns015xM
	13	86.2	2.9	685	13	BQ514325	BQ514325 EST621740
c	14	86	2.9	463	12	BJ093065	BJ093065 BJ093065
	15	86	2.9	671	12	BJ332362	BJ332362 BJ332362
c	16	84.6	2.8	606	12	BJ094042	BJ094042 BJ094042
c	17	84.6	2.8	608	12	BJ094122	BJ094122 BJ094122
	18	84.6	2.8	882	29	CNS07AEC	AL436474 T3 end of
	19	83.4	2.8	518	6	AU195980	Au195980 Porphyra
	20	83.4	2.8	552	6	AU194261	Au194261 Porphyra
	21	83.2	2.8	507	12	BM361364	BM361364 A00684-R
	22	83	2.8	582	12	BJ328707	BJ328707 BJ328707
	23	82.8	2.8	531	10	BG278090	BG278090 a1d12np.r
	24	82.2	2.7	598	29	CNS079O3	AL435529 T7 end of
	25	81.8	2.7	1040	29	CNS06D5J	AL393389 T3 end of
	26	81.6	2.7	677	14	CB629538	CB629538 OSIIEb05N
	27	81.6	2.7	813	14	CB629539	CB629539 OSIIEb05N
	28	80.8	2.7	660	13	BU873535	BU873535 Q056F03 P
c	29	79.6	2.6	676	28	BZ052416	BZ052416 jnr68f01.
	30	78.8	2.6	612	12	BJ331641	BJ331641 BJ331641
	31	78.4	2.6	540	13	BQ506197	BQ506197 EST613612
	32	77	2.6	615	12	BJ333781	BJ333781 BJ333781
	33	76.4	2.5	588	12	BJ304058	BJ304058 BJ304058
	34	76.2	2.5	735	14	CD458300	CD458300 Fg08_09f0
	35	76	2.5	613	12	BJ329654	BJ329654 BJ329654
c	36	75.8	2.5	739	14	CA932062	CA932062 MTU4TA.P2
	37	75.6	2.5	616	9	AI387759	AI387759 GH18412.5
	38	75.4	2.5	963	29	CNS06G9B	AL397413 T7 end of
	39	74.6	2.5	620	12	BJ339231	BJ339231 BJ339231
	40	74	2.5	597	12	BJ333289	BJ333289 BJ333289
	41	73.8	2.5	482	6	AU194918	Au194918 Porphyra
	42	73.8	2.5	544	6	AU194764	Au194764 Porphyra
	43	73.2	2.4	852	29	CNS06ULN	AL416001 T3 end of
	44	73	2.4	559	14	CD056225	CD056225 HO11J03S
	45	73	2.4	573	12	BJ323574	BJ323574 BJ323574